RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,693

DATE: 01/14/2002
TIME: 13:34:49

Input Set : A:\sequence 2613.txt
Output Set: N:\CRF3\01142002\J009693.raw

Does Not Comply
Corrected Diskette Needed

```
         2 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W-->     3 <120> TITLE OF INVENTION: Novel Protein and its DNA
W-->     4 <130> FILE REFERENCE: 2613WOOP
C-->     5 <140> CURRENT APPLICATION NUMBER: US/10/009,693
C-->     5 <141> CURRENT FILING DATE: 2001-12-10
         5 <150> PRIOR APPLICATION NUMBER: JP 11-163924
         6 <151> PRIOR FILING DATE: 1999-06-10
W-->     7 <160> NUMBER OF SEQ ID: 12
```

ERRORED SEQUENCES

```
       125 <210> SEQ ID NO: 3
       126 <211> LENGTH: 30
       127 <212> TYPE: DNA
       128 <213> ORGANISM: Artificial Sequence
W-->   129 <220> FEATURE:
       130 <223> OTHER INFORMATION: Primer
E-->   131 <400> SEQUENCE: 30
C-->   132 ggtgggatgg ataacagggt ctcgggaacg                          30
       197 <210> SEQ ID NO: 12
       198 <211> LENGTH: 36
       199 <212> TYPE: DNA
       200 <213> ORGANISM: Artificial Sequence
W-->   201 <220> FEATURE:
       202 <223> OTHER INFORMATION: Primer
W-->   203 <400> SEQUENCE: 12
C-->   204 tcaccagtcg acggcacaca ggcaccatcc aagggc                    36
E-->   210 (1/8) delete
```

VERIFICATION SUMMARY　　　　　　　　DATE: 01/14/2002
PATENT APPLICATION:　US/10/009,693　　TIME: 13:34:50

Input Set : **A:\sequence 2613.txt**
Output Set: **N:\CRF3\01142002\J009693.raw**

```
L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:7 M:283 W: Missing Blank Line separator, <160> field identifier
L:8 M:283 W: Missing Blank Line separator, <210> field identifier
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:129 M:283 W: Missing Blank Line separator, <220> field identifier
L:131 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:30
L:131 M:283 W: Missing Blank Line separator, <400> field identifier
L:132 M:112 C: (48) String data converted to lower case,
L:137 M:283 W: Missing Blank Line separator, <220> field identifier
L:139 M:283 W: Missing Blank Line separator, <400> field identifier
L:140 M:112 C: (48) String data converted to lower case,
L:145 M:283 W: Missing Blank Line separator, <220> field identifier
L:147 M:283 W: Missing Blank Line separator, <400> field identifier
L:148 M:112 C: (48) String data converted to lower case,
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:155 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:112 C: (48) String data converted to lower case,
L:161 M:283 W: Missing Blank Line separator, <220> field identifier
L:163 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:112 C: (48) String data converted to lower case,
L:169 M:283 W: Missing Blank Line separator, <220> field identifier
L:171 M:283 W: Missing Blank Line separator, <400> field identifier
L:172 M:112 C: (48) String data converted to lower case,
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:179 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:112 C: (48) String data converted to lower case,
L:185 M:283 W: Missing Blank Line separator, <220> field identifier
L:187 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:112 C: (48) String data converted to lower case,
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:112 C: (48) String data converted to lower case,
L:201 M:283 W: Missing Blank Line separator, <220> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:204 M:112 C: (48) String data converted to lower case,
L:210 M:254 E: No. of Bases conflict, LENGTH:Input:8 Counted:37 SEQ:12
L:210 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:210 M:252 E: No. of Seq. differs, <211>LENGTH:Input:36 Found:37 SEQ:12
```